

10/539450

Figure 1

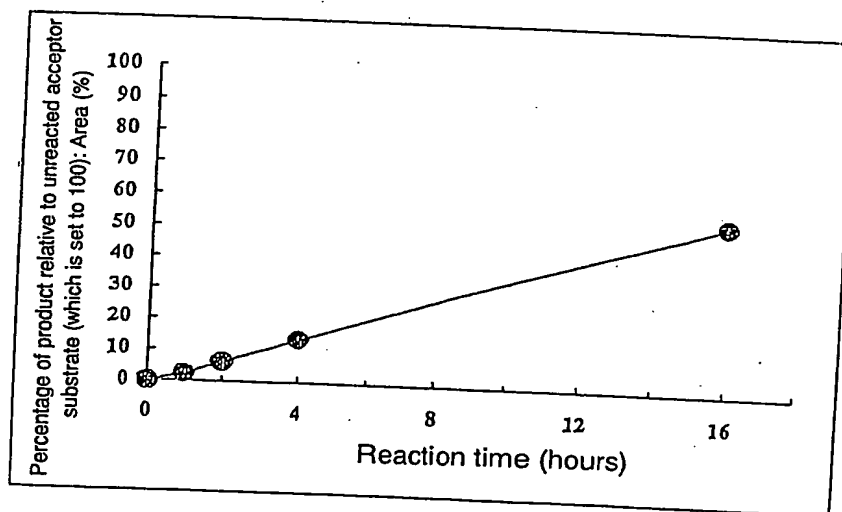


Figure 2A

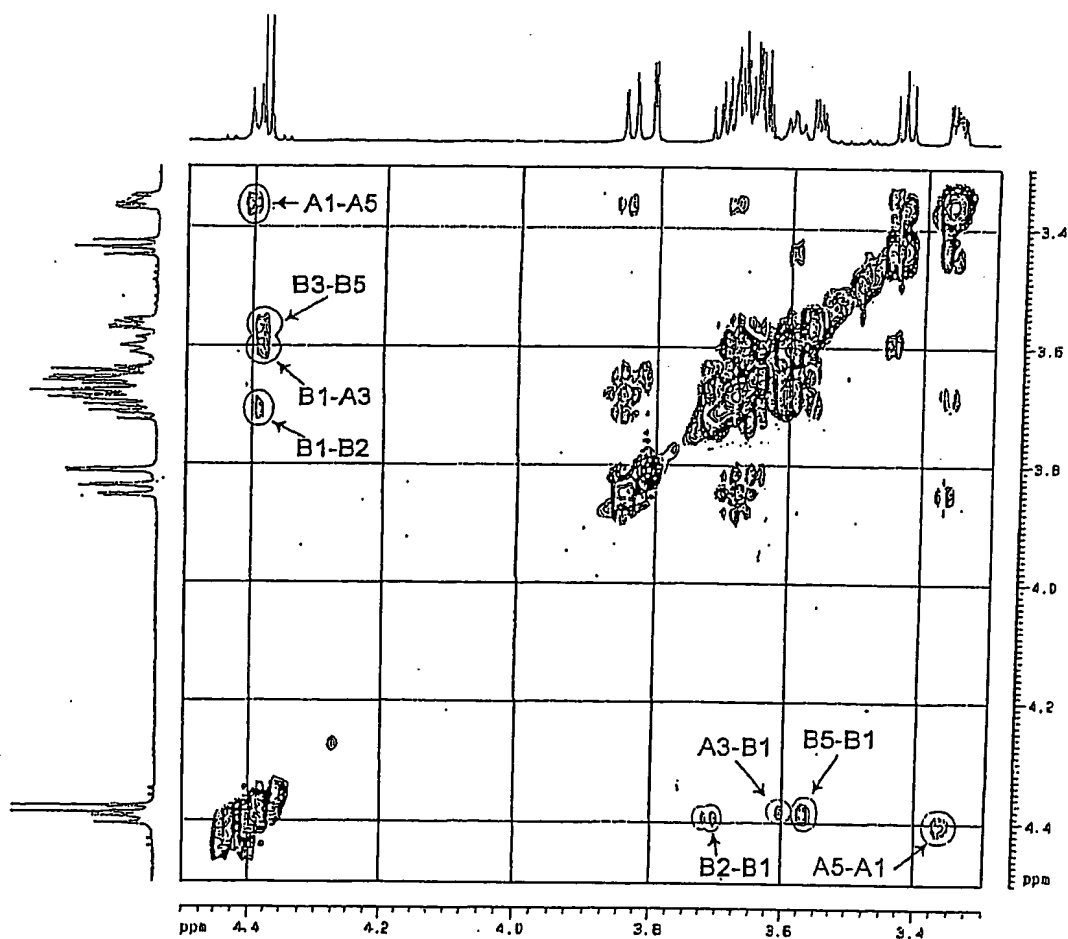


Figure 2A (continued)

G34, noesyprtp, 0.9s, 298K, 03-01-09

Current Data Parameters

NAME	G34
EXPNO	9
PROCNO	1

F2 - Acquisition Parameters

Date_	20021228
Time	12.12
INSTRUM	dmx750
PROBHD	5 mm 1H XYZ-
PULPROG	noesyprtp
TD	2048
SOLVENT	D2O
NS	16
DS	16
SWH	6009.615 Hz
FIDRES	2.934382 Hz
AG	0.1704436 sec
RG	2048
DW	83.200 usec
DE	4.50 usec
TE	300.0 K
d0	0.00000300 sec
D1	1.39999998 sec
D8	0.89999998 sec
d11	0.03000000 sec
d12	0.00002000 sec
d13	0.00000300 sec
INO	0.00008331 sec

***** CHANNEL f1 *****

NUC1	1H
P1	8.65 usec
PL1	1.00 dB
PL9	75.00 dB
SFO1	750.1335265 MHz

F1 - Acquisition parameters

ND0	2
TD	512
SFO1	750.1335 MHz
FIDRES	11.721681 Hz
SW	8.001 ppm

F2 - Processing parameters

SI	1024
SF	750.1299973 MHz
WOW	QSINE
SSB	2
LB	0.00 Hz
GB	0
PC	1.00

F1 - Processing parameters

SI	1024
WC2	TPPI
SF	750.1299974 MHz
WOW	QSINE
SSB	2
LB	0.00 Hz
GB	0

2D NMR plot parameters

CX2	15.00 cm
CX1	15.00 cm
F2PLO	4.500 ppm
F2LO	3375.58 Hz
F2PHI	3.300 ppm
F2HI	2475.43 Hz
F1PLO	4.500 ppm
F1LO	3375.58 Hz
F1PHI	3.300 ppm
F1HI	2475.43 Hz
F2PPNCN	0.08000 ppm/cm
F2HZCN	60.01040 Hz/cm
F1PPNCN	0.08000 ppm/cm
F1HZCN	30.01040 Hz/cm

Figure 2B

NOESY mixing time 900ms

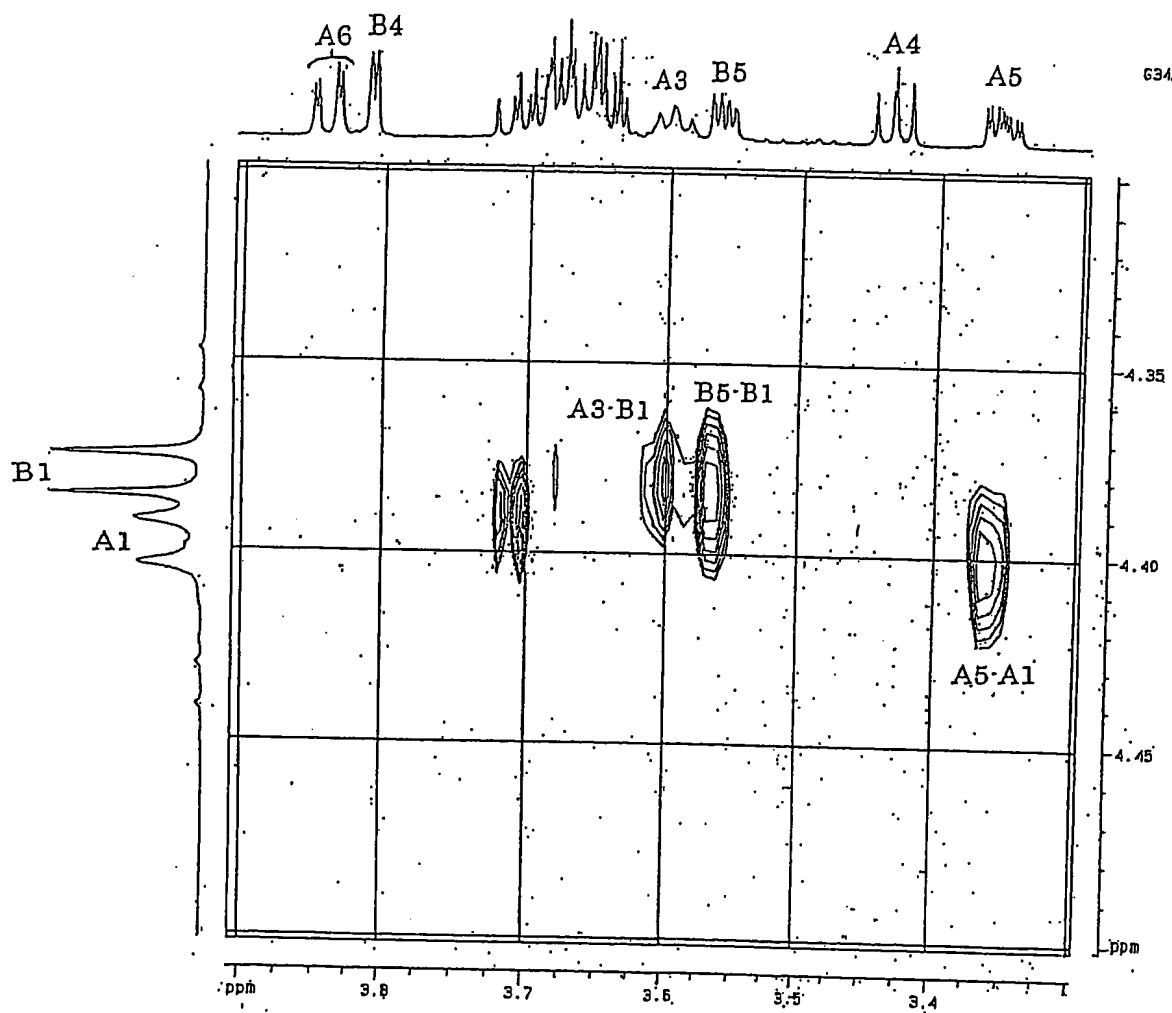


Figure 2B (continued)

G34, noesyprtp, 0.9s, 298K, 03-01-09

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Current Data Parameters
NAME          G34
EXPNO         9
PROCNO        1

F2 - Acquisition Parameters
Date_         20021228
Time          12.12
INSTRUM       dmx750
PROBHD        5 mm 1H XYZ-
PULPROG       noesyprtp
TD            2048
SOLVENT       D2O
NS            16
DS            16
SWH           6009.615 Hz
FIDRES        2.934382 Hz
AQ            0.1704436 sec
RG            2048
DW            83.200 usec
DE            4.50 usec
TE            300.0 K
d0            0.00000300 sec
d1            1.39999998 sec
d8            0.89999998 sec
d11           0.03000000 sec
d12           0.00002000 sec
d13           0.00000300 sec
INO           0.00008331 sec

***** CHANNEL f1 *****
NUC1           1H
P1             8.65 usec
PL1            1.00 dB
PL9            75.00 dB
SF01          750.1335265 MHz

F1 - Acquisition parameters
ND0            2
TD             512
SF01          750.1335 MHz
FIDRES        11.721681 Hz
SW             8.001 ppm

F2 - Processing parameters
SI            1024
SF            750.1299973 MHz
WOW           QSINE
SSB           2
LB            0.00 Hz
GB            0
PC            1.00

F1 - Processing parameters
SI            1024
WC2           TPPI
SF            750.1299974 MHz
WOW           QSINE
SSB           2
LB            0.00 Hz
GB            0

2D NMR plot parameters
CX2           15.00 cm
CX1           15.00 cm
F2PLO         8.907 ppm
F2LO          2930.51 Hz
F2PHI         3.296 ppm
F2HI          2472.75 Hz
F1PLO         4.501 ppm
F1LO          3376.70 Hz
F1PHI         4.298 ppm
F1HI          3224.32 Hz
F2PPNCN       0.04068 ppm/cm
F2HZCN        30.51759 Hz/cm
F1PPNCN       0.01354 ppm/cm
F1HZCN        10.15880 Hz/cm

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10/539458

Figure 3

Table 1

¹ H Chemical shift	A (ppm)	B (ppm)
δ1	4.398*	4.381*
δ2	3.687	3.711*
δ3	3.599*	3.655
δ4	3.435*	3.811*
δ5	3.358*	3.562*
δ6	3.681	3.645
δ6	3.844*	3.698
δCH ₃	1.828*	1.892*

Table 2

Coupling coefficient	A (Hz)	B (Hz)
J12	8.4	8.4
J23	9.8	10.6
J34	8.6	5.9
J45	9.2	3.3?
J56a	5.8	5.5
J56b	2.2	4.0
J6a6b	12.4	12.1

Figure 4

Table 3

f2	Signal	f1	Signal	300 ms	600 ms	900 ms
7.265	phenyl	1.828	CH ₃	-	w	w
7.265	phenyl	4.557	CH ₂ (high)	w	m	m
7.265	phenyl	4.778	CH ₂ (low)	w	m	m
7.265	phenyl	4.398	A1	-	-	m
4.557	CH ₂	4.398	A1	-	w	m
4.398	A1	4.557	CH ₂	-	w	w
4.398	A1	3.358	A5	-	m	m
4.381	B1	3.599	A3	-	w	m
4.381	B1	3.562	B5	-	m	m
3.599	A3	4.381	B1	-	w	m
3.562	B5	4.381	B1	-	m	s
3.358	A5	4.398	A1	-	m	m

Figure 5

B3Gal-T1 1: FLVILISTTHKEFDARQAI RETWGDENNFKG1K-IA-T-IFLLG---KNAD--PVL---- 48
 B3Gal-T2 1: FLILLIAAEPQIEARRAIRQTWGNESLAPG1Q-IT-R-IFLLGLSIKEN---GYL---- 50
 B3Gal-T3 1: FLVILVTSHPSDVKAARQAI RVTWGEKKSWWGYE-VL-T-IFLLGQEA EKED--KML---- 51
 B3Gal-T5 1: FLVLLVTSSHKQLAHRMAIRQTWGERMYKQKQ-LK-T-IFLLGTTSSAAE--T----- 49
 B3Gal-T6 1: FLAVLVASAPRAAEHRSVIRSTWLARRGAPGD--VWAR--FAVGTAGLGAE--ER----- 49
 G34 1: DVVVGVL SARNNHLELRNVIRSTWMRHLLQHPTLSQRVLVKFI IGAHGCEVPVEDREDPYS 60
 * * * * * M1 * *
 B3Gal-T1 49: -N----- 49
 B3Gal-T2 51: -Q----- 51
 B3Gal-T3 52: -A----- 52
 B3Gal-T5 50: ----- 50
 B3Gal-T6 50: ----- 50
 G34 61: CKLLNITNPVLNQEI EAFSLSEDTSSGLPEDRVVSVSFRVLYPIVITSLGVFYDANDVGF 120
 B3Gal-T1 50: ----- 50
 B3Gal-T2 52: ----- 52
 B3Gal-T3 53: ----- 53
 B3Gal-T5 50: ----- 50
 B3Gal-T6 50: ----- 50
 G34 121: QRNITVKLYQAEQEALFIARFSPSCGVQVKNLWYKPVEQF ILPESFEGTIVWESQDLH 180
 B3Gal-T1 50: ----- 50
 B3Gal-T2 52: ----- 52
 B3Gal-T3 53: ----- 53
 B3Gal-T5 50: ----- 50
 B3Gal-T6 50: ----- 50
 G34 181: GLVSRNLHKVTVNDGGGVL RVITAGEGALPHEFLEGVEGVAGGFIYTIQEGDALLHNLHS 240
 B3Gal-T1 50: -----QMVEQESQIFHDIIVE-DFIDSYHNLTLKTLMGMRWVATFCSKA 92
 B3Gal-T2 52: -----RAILEESRQYHDI IQQ-EYLDITYNLTIKTLMGMWVATYCPHI 94
 B3Gal-T3 53: -----LSLEDEHLLYGDIIRO-DFLDITYNLTIKTLMAFRWVTEFCPNA 95
 B3Gal-T5 50: -----KEVDQESQRHGDIIQK-DFLDVYYNLTIKTMMGIEWVHRFCPOA 92
 B3Gal-T6 50: -----RALEREQARHGDL LLLPALRDAYENLTAKVLA MLAWLDEHVAF- 92
 G34 241: RPQRLIDHIRNLHEEDALLKEESSIYDDIVFV-DVVDYTRNVPKLLNFYRWVETTSFN 299
 * * * * * M2 * * * * *
 B3Gal-T1 93: KYVMKTDSDIFVNMNLIYKLLKPSTKPRRYFTGYVINGG---P-IRDVRSKWYMPRDL 148
 B3Gal-T2 95: FYVMKTDSDMFVNT EYLJNKLLKPDLPFRHNYFTGYLMRGYA--P-NRNKDSKWYMPDL 151
 B3Gal-T3 96: KYVMKTDTDVFI NTGNLVKYLNLNHSEKF--FTGYPLIDNY--S-YRGFYQKTHISYQE 150
 B3Gal-T5 93: AFVMKTDSDMFINVDYLT ELLKKNRTTRF--FTGFLKLN EF--P-IRQPFKWFVSKSE 147
 B3Gal-T6 93: EFVLKADDDSFARLDALLAELRAREPARRRRLYWGFFSGRGRVKPGGRWREA AWQLCD-- 150
 G34 300: LLLKTDDDCYIDLEAVFNRI VQKNLDGPNF-WWGNFRLNWAV---DRT--GKWQEL--E 350
 * * * * *
 B3Gal-T1 149: YPDSNYP PF-CSGTGYIFSADVAELIYKTS LHTRLHLEDVYVGLCLRKLG1HPFQON-SG 206
 B3Gal-T2 152: YPSERYPVF-CSGTGYVFSGLAEKIFKVS LGIRRLHLEDVYVGLCLAKLRIDPVPPPNE 210
 B3Gal-T3 151: YPFKVFPFY-CSGLGYIMSRDLVPRIYEMMGHVKPIKFEDVYVGLCLNLLKVNHIH1PEDT 209
 B3Gal-T5 148: YPWDRYP PF-CSGTGYVFSGDVASQVYNVSKSVPIKLEDVYVGLCLERLNI RLEELHSQ 206
 B3Gal-T6 151: YYL---PYAL--GGGYVLSADLVHYLR LSRDYLRAWHSEDVSLGAWLA--PVDVQREHD- 202
 G34 351: YPSPAYPAFAC-GSGYVISKDIVKWLASNSGR LKTYQGEDVSMGIYMAAIGPKRYQD-SL 408
 * * * * * M3 * * * * *
 B3Gal-T1 207: --FNHWMAYSLCRYRRVITVHQISPEEMHRIWN DMSSKKHLRC----- 248
 B3Gal-T2 211: FVFNHWRVSYSSCKYSHLITSHQFQPS ELIKYWNHLOQNKHNACANA AKEKA----- 262
 B3Gal-T3 210: NLFFLYRIHL DVCQLRRVIAAHGFSSKEIITFWQVMLRN--TTCHY----- 253
 B3Gal-T5 207: PTFPPGGLRFSVCLFRRI VACHFIKPR TLLDYWQALENSRGEDCP-PV----- 253
 B3Gal-T6 203: PRFDTE-YRSRGCSNOYL VTHKQ-SLEDMLEKHATL-AREGR LCKREVQLRLSYVYDWSA 259
 G34 409: -----WLC-EKTCETGMLSSP-QYSPWELTELWK-LKERC GDPC-RC-QAR----- 449
 * * * * *
 B3Gal-T1 249: ----- 249
 B3Gal-T2 263: -----GRYRHRKLH- 271
 B3Gal-T3 254: ----- 254
 B3Gal-T5 254: ----- 254
 B3Gal-T6 260: PPSQCCQR-REGIP 272
 G34 450: ----- 450

Figure 6

M 1

b3GnT2	FLLLAIKSLTPHFARRQAIRESWQES-NAGNQT---VVRVFLGQTPPEDNHP-DLSDM
b3GnT3	FLLLVIKSSPSNYVRRELLRRTWGRER-KVRGLQ---LRLFLVGTASNPHEAR-KVNRL
b3GnT4	FLLLAIKSQPGHVERRAAIRSTWGRVGGWARGRQ---LKLVLFLGVAG---SA-PPAQL
b3GnT5	LLLLFVKTAPENYDRRSIGIRRTWGNEN-YVRSQLNANIKTLFALGTPNPLE-GE-ELQRK
b3Gal-T6	FLAVLVASAPRAVERRTAVRSTWLAPE-RRGGPED--VWARFAVGTGGGGS---EERRA
hGal-T1	FLVILISTTHKEFDARQAIRETWGNEN-NFKGIK---IATLFLGKNADP---VLNQM
hGal-T2	FLILLIAAEPGQIEARRAIRQTWGNES-LAPGIQ---ITRIFLLGLSIKLN--G-YLQRA
hGal-T3	FLVILVTSHPSDVKARCAIRVTWGEKK-SWNGYE---VLTFFLLGQAEKE-DK-MLALS
hGal-T4	FLLLIVCTAPENLNQRNAIRASWGLR-EARGLR---VQTLFLLGEPNAQHPVWGSQGS
hGal-T5	FLVLLVTSSHKQLAERMAIRQTWGER-MVKGKQ---LKTFFLLGTTSSA---AETKE

M 2

b3GnT2	LKFESEKHQDILMW-NYRDTFFNLSLKEVFLRWVSTSCPDTEFYFKGDDVFNTHHIL
b3GnT3	LELEAQTHGDILQW-DFHDSFFNLTLKQVFLQWQETRCANAFVNLGDDVFAHTDNMV
b3GnT4	LAYESREFDDILQW-DFTEDFNLTLKELHLQRWVVAACPAHFMLKGDDVFNHVPNVL
b3GnT5	LAWEDQRYNDIIQ-DFVDSFYNLTLLMQFSWANTYCPHANFLMTADDIFIHMPNLI
b3Gal-T6	LELEQAQHGDLILLPALRDAYENLTAKVLAMLTWLDER-VDFEVLKADDDSFARLDAIL
hGal-T1	VEQESQIFHDIIVE-DFIDSYHNLTLLTLMGMRWVATFCSKANYMKTDSDFVNMDNLI
hGal-T2	ILEESRQYHDIQ-ELYDTYNNLTIKTLMGMWVATYCPHIFVMKTDSDFVNTYELI
hGal-T3	LEDEHLLYGDIIRQ-DFLDTYNNLTIKTMAFRWVTEFCPNAHYVMKTDTDYFINTGNLV
hGal-T4	LASESAAQGDILQA-AFQDSYRNLTLLTSLGNWAEKHCPMARYVLKTDDVYVNPVELV
hGal-T5	VDQESQRHGDIIQK-DFLDVYNNLTLLTMMGIEWVHRFCPQAAEVMKTDSDFINVDYLT

M 3

b3GnT2	NYLNS-----LSKTKAKDLFIGDVIHNAGPHRDKKLKYYI
b3GnT3	FYLDQ-----HDP--GRHLFVGQLIQNVGPIRAFWSKYYV
b3GnT4	EFLDG-----WDP--AQDLLVGDVIRQALPNRNTKVYFI
b3GnT5	EYLS-----LEQIGVQDFWIGRVHRGAPPIRDKSSKYYV
b3Gal-T6	VDLRA-----REPARRRRLYWGFFSGR--GRVKPGGRWRE
hGal-T1	YKLLK-----PSTKPRRYFTGYVING-GPIRDVRSKWYM
hGal-T2	NKLLK-----PDLPPRHNYFTGYLMRGYAPNRNKDSKWYM
hGal-T3	KYLLN-----LNH--SEKFFTGYPLIDNYSYRGFYQKTHI
hGal-T4	SELVLRGGRWGQWERSTEPQREAEQGGQVLHSEEVPLLYLGRVHWRVNPSTPGGRHRV
hGal-T5	ELLLK-----KNR--TTRFFTGLKLNEFPRIQPFKSWFV

M 3

b3GnT2	PEVVYSG---LYPPYAGGGGFLYSGHIALRLYHITDQVH-LYPIDDVYTGMLQKLGVLV
b3GnT3	PEVVTQNE--RYPPYCGGGGFLSRFTAALRAAHVLD-IFPIDDVFLGMLGLEGLKP
b3GnT4	PPSMYRAT--HYPPYAGGGGYMSRATVRRLOAIMEDAE-LFPIDDVFGMLRRLGLSP
b3GnT5	SYEMYQWP--AYPDYTAGAAYVISGDVAAKVYEASQTLNSSLYDDVFMGLANKIGIVP
b3Gal-T6	AAWQLCD---YYLPYALGGGYLSADLVHYLRLSREYLR-AWHSEPVSLGTWAPVDVQR
hGal-T1	PRDLYPDS--NYPPFCSGTGYIFSADVAELIYKTSLHTR-LLHLEDVYVGLRLKLGHP
hGal-T2	PPDLYPSE--RYPVFCSGTGYVFSGDLAEKIFKVSIGIR-RLHLEDVYVGLAKLRIDP
hGal-T3	SYQEYPFK--VFPPYCSGLGYMSRDLVPRIYEMMGHVK-PIKFEDVYVGLNLLKVNI
hGal-T4	SEEQWPHTWGPFPYASGTGYLSASAVQLIKVASRAP-LLPLEDVFGVSARRGGLAP
hGal-T5	SKSEYPWD--RYPPFCSGTGYVFSGDVASQYVNSKSVY-YIKLEDVFGVGLERLNIRL

b3GnT2	EKHKGFRFTDIE-----EKNKNNICSYVDLMLVHSRKPQEMIDIWSQLQSA-----
b3GnT3	ASHSGIRTSGVRAPSQHLSSEDFPCFYRDLLVHRLPYEMLMWDALNQP-----
b3GnT4	MHHAGFKTFGIIR---PLDPLDPCLYRGLLVHRLSPLEMWMTMWALVTDE-----
b3GnT5	QDHVFFS--GEGK-----TPYHPCIEKMMTSHG-HLEDQLWKNATDPKVKTKSGFF
b3Gal-T6	EHDPRFD--TEYK-----SRGCNNQYLVTBKQ-SPEDMLEKQMLLHEG-----

Note: "b3" represents a β 1,3 linkage and "Gn" represents GlcNAc.

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Figure 7

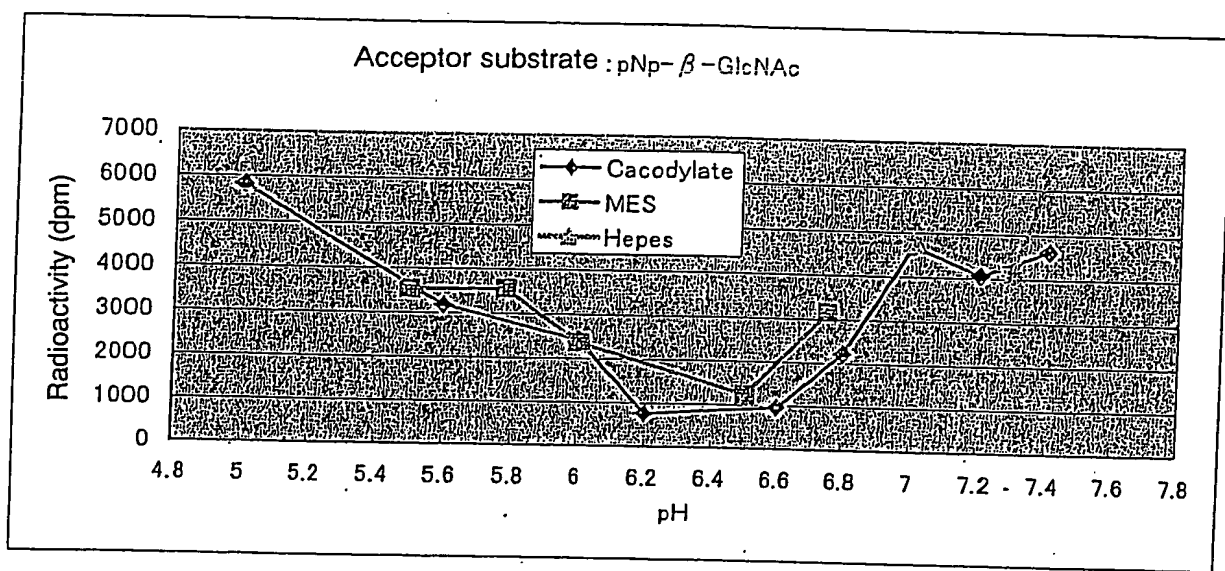


Figure 8

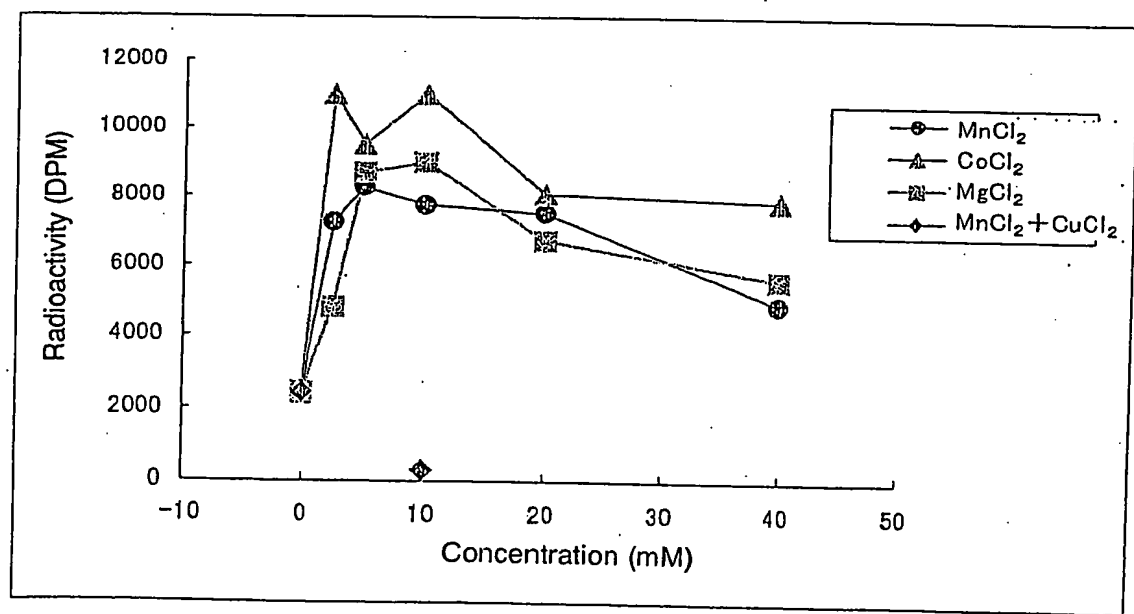


Figure 9

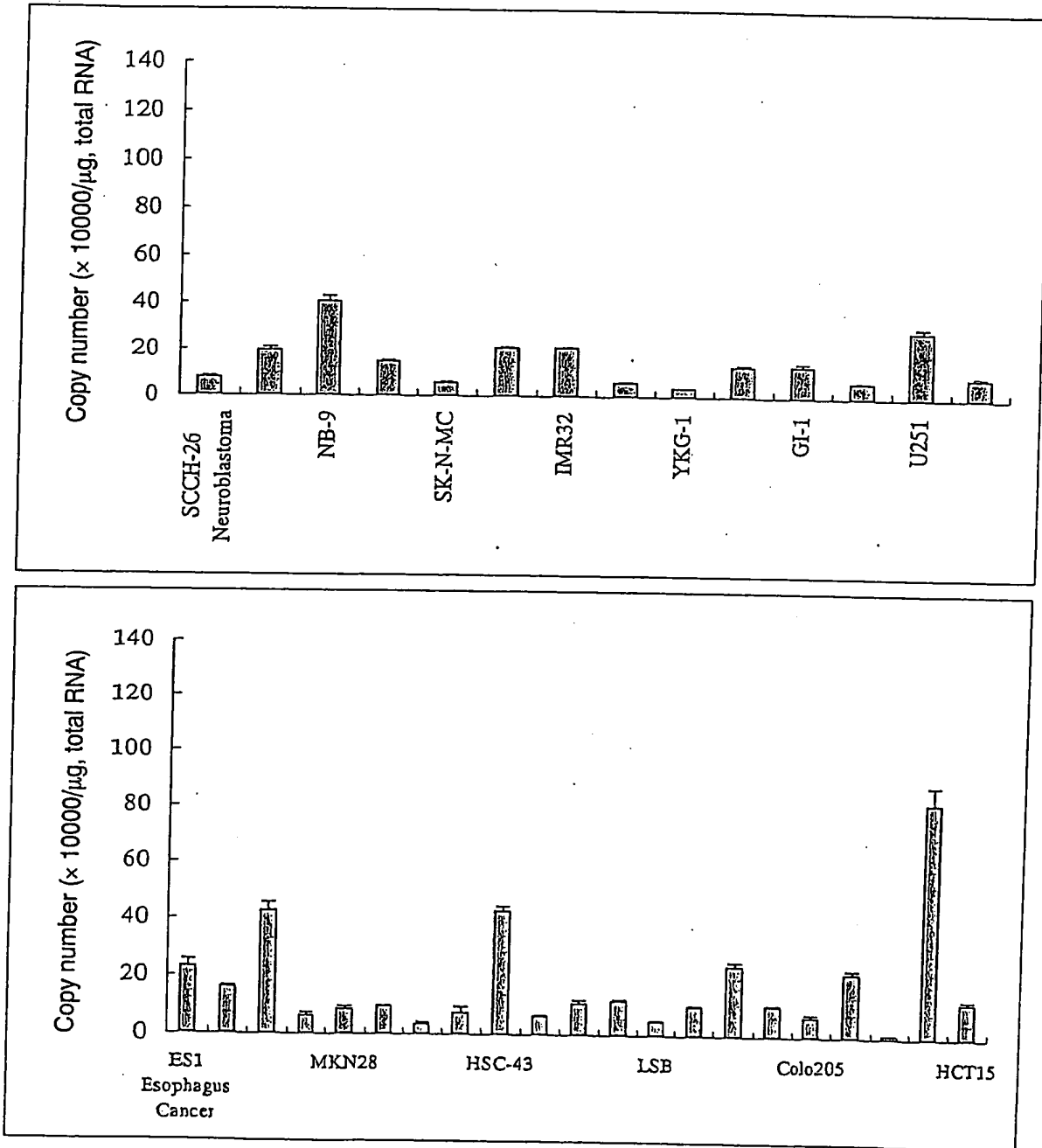


Figure 9 (continued)

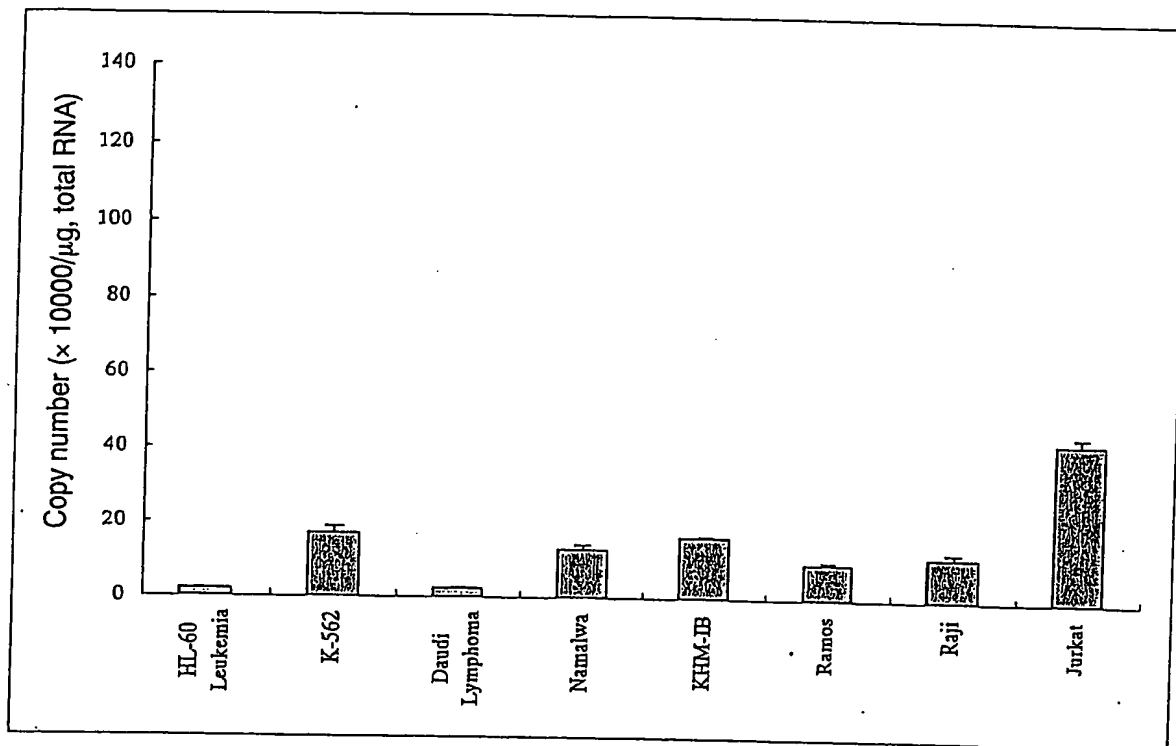


Figure 9 (continued)

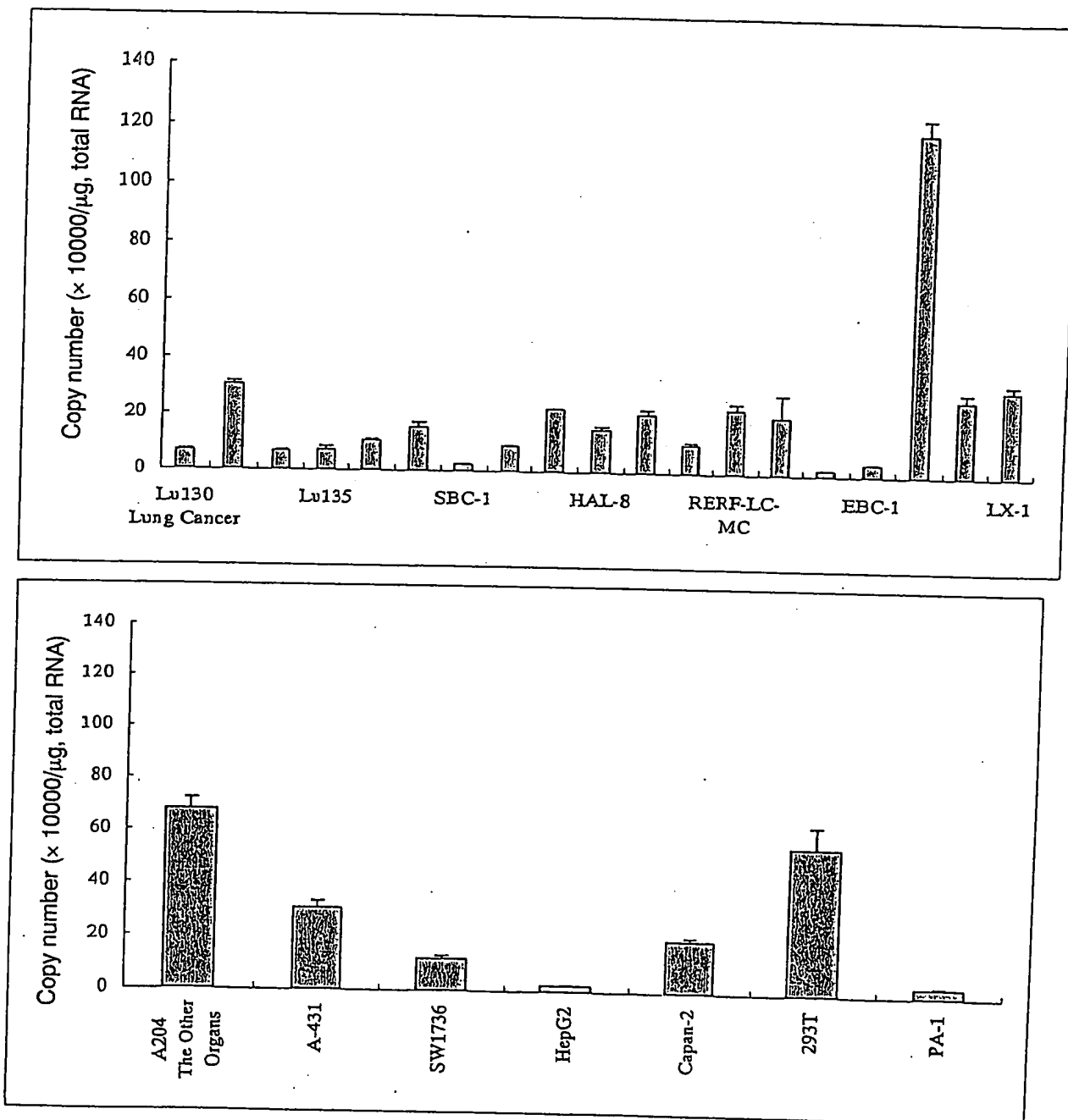


Figure 9 (continued)

	Cell Line	Copy number (x 10000 /μg, total RNA)	
Neuroblastoma	SCCH-26	7.87	0.59
	NAGAI	19.53	1.45
	NB-9	40.56	2.34
	SK-N-SH	14.93	0.74
	SK-N-MC	5.79	0.47
	NB-1	20.90	0.54
	IMR32	21.03	0.25
Glioblastoma	T98G	6.20	0.24
	YKG-1	3.85	0.05
	A172	13.38	0.87
	GI-1	13.72	1.25
	U118MG	6.80	0.51
	U251	28.90	1.89
Lung Cancer	KG-1-C	9.09	0.55
	Lu130	6.80	0.42
	Lu134A	30.31	1.16
	Lu134B	6.76	0.40
	Lu135	7.16	1.32
	Lu139	10.66	0.50
	Lu140	15.36	1.83
	SBC-1	2.46	0.22
	PC-7	9.08	0.20
	PC-9	22.42	0.11
	HAL-8	15.18	1.22
	HAL-24	20.80	1.71
	ABC-1	10.27	0.87
	RERF-LC-MC	22.85	2.15
	EHHA-9	20.34	7.88
	PC-1	2.13	0.18
	EBC-1	4.41	0.19
	PC-10	118.76	4.89
	A549	27.10	2.63
	LX-1	30.72	2.06
Esophagus Cancer	ES1	23.03	2.53
	ES2	16.07	0.65
	ES6	42.76	2.96
Gastric Cancer	MKN1	6.20	1.10
	MKN28	8.56	0.99
	MKN7	9.71	0.10
	MKN74	3.46	0.81
	MKN-45	7.32	2.13
	HSC-43	42.82	1.67
	KATOIII	6.37	0.37
	TMK-1	10.78	1.19
Colorectal Cancer	LSC	11.76	0.57
	LSB	4.89	0.30
	SW480	10.05	0.43
	SW1116	24.09	1.39
	Colo201	10.40	0.41
	Colo205	6.80	0.88
	C1	21.86	1.20
	WiDr	1.24	0.04
	HCT8	82.17	6.24
	HCT15	12.14	0.96
The Other Organs	A204	67.94	4.37
	A-431	30.59	2.52
	SW1736	11.92	1.13
	HepG2	2.27	0.35
	Capan-2	19.43	1.24
	293T	55.14	8.29
	PA-1	3.52	0.56
Leukemia	HL-60	2.08	0.11
	K-562	17.08	1.77
Lymphoma	Daudi	2.41	0.20
	Namalwa	13.00	1.20
	KHM-IB	16.35	0.45
	Ramos	9.54	0.75
	Raji	11.56	1.31
	Jurkat	42.71	1.93
	YKN45	10.12	0.56

Figure 10

```

mouse G34 1' MRNWLVLCP CVLGAALHLW HLWLRSPDP HNTGPSAADQ SALFEHWKFS HYDVVVGVL
*****
human G34 1" MRNWLVLCP CVLGAALHLW -LRLRSPPPA CASGAGPADQ LALFPQWKST HYDVVVGVL
*****
61' ARNNHELNV IRNTWLKNLL HHPTLSQRL VKFIIGARGC EVFVEDREDP YSCRLNITN
*****
60" ARNNHELNV IRSTWMRHLL QHPTLSQRL VKFIIGARGC EVFVEDREDP YSCKLLNITN
*****
121' PVLNQIEAF SFPEDASSR LSEDRVSVS FRVLYPIVIT SLGVFYDASD VGFQRNITVK
*****
120" PVLNQIEAF SLSEDTS5G- LPEDRVSVS FRVLYPIVIT SLGVFYDAND VGFQRNITVK
*****
181' LYQTEQEEAL FIARFSPSC GVQVKNLWYK PVEQFILPES FEGTIVWESQ DLHGLVSRNL
*****
179" LYQAEQEEAL FIARFSPSC GVQVKNLWYK PVEQFILPES FEGTIVWESQ DLHGLVSRNL
*****
241' HRVTVNDGGG VLRVLAAGEG ALPHEFMEGV EGVAGGFIYT VQEGDALLRS LYSRQRLAD
*****
239" HKVTVNDGGG VLRVITAGEG ALPHEFLEGV EGVAGGFIYT IQEGDALLHN LHSRQRLID
*****
301' HIQDLQVEDA LLQEESSVHD DIVFVDVVDT YRNVPKLLN FYRWTVESTS FDLLLKTDDD
*****
299" HIRNLHEEDA LLKEESSIYD DIVFVDVVDT YRNVEAKLLN FYRWTVETTS FNLLLKTDDD
*****
361' CYIDLEAVFN RIAQKNLDGP NFWWGNFRLN WAVDRTGKWQ ELEYPSPAYP AFACGSGYVI
*****
359" CYIDLEAVFN RIVQKNLDGP NFWWGNFRLN WAVDRTGKWQ ELEYPSPAYP AFACGSGYVI
*****
421' SKDIVDWLAG NSRRLKTYQG EDVSMGIWMA AIGPKRHQDS LWLCEKTCET GMLSSPOYSP
*****
419" SKDIVKWLAS NSGRLKTYQG EDVSMGIWMA AIGPKRYQDS LWLCEKTCET GMLSSPOYSP
*****
461' EELSKLWELK ELCGDPCQCE AKVR
*****
479" WELTELWKLK ERCGDPCRCQ AR
*****

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Figure 11

